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up to the full length of a probe derived from the cDNA sequence shown in SEQ ID NO:1 or SEQ ID NO:7 or SEQ ID NO: 12 or SEQ ID NO: 15 or SEQ ID NO: 16 and isolating a nucleotide sequence which has promoter activity from the 5' flanking region of genomic DNA which specifically hybridizes to said probe, wherein hybridization is carried out in a solution comprising 50% formamide, 5X SSC, 0.1% SDS, 5 mM EDTA, 10X Denhardt's solution, and 25 mM sodium phosphate at pH 6.5 with 250 µg/ml carrier DNA, and hybridization washes are performed in 2X SSC, 0.1% SDS at 42°C for 3 x 30 minutes, whereby said transcriptional factor is obtained.

2. (Reiterated) The DNA sequence according to Claim 1, further comprising a transport signal encoding sequence from a plant nuclear-encoded gene.
3. (Reiterated) The DNA sequence according to Claim 2, wherein said transport signal encoding sequence comprises a plastid transit peptide.
4. (Reiterated) The DNA sequence according to Claim 1, wherein said DNA sequence further comprises as an operably joined component a transport signal encoding sequence for a signal peptide which provides for transport across the rough endoplasmic reticulum.
5. (Reiterated) The DNA sequence according to Claim 4, wherein said DNA sequence further comprises as an operably joined component, 3' to said open reading frame, a vacuolar localization signal.
7. (Reiterated) The DNA sequence of Claim 1 wherein said open reading frame is from a bacterial or a plant gene.
8. (Reiterated) The DNA sequence of Claim 7 wherein said gene is selected from the group consisting of ORF438, *tyrA*, anthocyanin R gene, anthocyanin C1 gene, *pig*, and *tma*.

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9. (Reiterated) A DNA construct comprising a DNA sequence of Claim 1.
10. (Reiterated) A DNA construct comprising two DNA sequences according to Claim 1, wherein said protein in a biosynthesis pathway in each of said two DNA sequences is not encoded by the same gene.
12. (Reiterated) A plant cell comprising a DNA construct of Claim 9.
13. (Reiterated) A plant comprising a cell of Claim 12.
14. (Reiterated) A method of modifying fiber phenotype in a cotton plant, said method comprising:
  - transforming a plant cell with a DNA construct according to Claim 9 or 10; and
  - growing said plant cell to produce a plant comprising said fiber tissue, wherein said plant tissue comprises a substrate of said protein of interest, and wherein said protein reacts with said substrate to produce said pigment, whereby the phenotype of said fiber is modified.
15. (Reiterated) The method of Claim 14 wherein said DNA construct further comprises a transport signal encoding sequence from a plant nuclear-encoded gene.
16. (Reiterated) The method of Claim 14 wherein said DNA construct further comprises a transport signal encoding sequence, which encodes a signal peptide which provides for transport across the rough endoplasmic reticulum.
18. (Reiterated) The method of Claim 16 wherein said DNA comprises constructs for expression of two proteins in a pigment biosynthesis pathway wherein said two proteins are not encoded by the same gene.

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19. (Reiterated) The method of Claim 18 wherein said pigment is melanin and said proteins are encoded by *tyrA* and ORF438.
20. (Reiterated) The method of Claim 18 wherein said pigment is indigo and said proteins are encoded by *tna* and *pig*.
21. (Reiterated) The method of Claim 18 wherein said pigment is anthocyanin and said two proteins are the anthocyanin R and C1 proteins.
22. (Reiterated) The method of Claim 14 wherein said fiber tissue is a cotton burr.
23. (Reiterated) A recombinant DNA construct comprising the cotton tissue transcriptional sequence shown in SEQ ID NO: 7.
24. (Reiterated) A recombinant DNA construct comprising the cotton tissue transcriptional sequence shown in SEQ ID NO: 15.
25. (Reiterated) An isolated DNA comprising the nucleotide sequence shown in SEQ ID NO: 1.
26. (Reiterated) An isolated DNA comprising the nucleotide sequence shown in SEQ ID NO: 12.
27. (Reiterated) The method of Claim 14 wherein said protein is an enzyme in the biosynthetic or degradation pathway of a plant pigment.

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28. (Reiterated) The DNA sequence according to Claim 1 wherein said plant fiber tissue is cotton fiber tissue.

Cancel Claim 29 and rewrite as new Claim 58.

*Sub F12* 30. (Amended) The DNA sequence according to Claim [30] 59, further comprising a transport signal encoding sequence from a plant nuclear-encoded gene.

31. (Reiterated) The DNA sequence according to Claim 30, wherein said transport signal encoding sequence comprises a plastid transit peptide.

*Sub F14* 32. (Amended) The DNA sequence according to Claim [30] 59, further comprising a transport signal encoding sequence for a signal peptide which provides for transport across the rough endoplasmic reticulum.

33. (Reiterated) The DNA sequence according to Claim 32, wherein said sequence further comprises, 3' to said open reading frame, a vacuolar localization signal.

34. (Reiterated) The DNA sequence of Claim 57 wherein said open reading frame is from a bacterial gene.

35. (Reiterated) The DNA sequence of Claim 34 wherein said gene is selected from the group consisting of ORF438, *tyrA*, *pig*, and *tna*.

*Sub F16* 36. (Amended) A DNA construct comprising a DNA sequence of Claim [30] 59.

37. (Reiterated) The DNA construct of Claim 36 wherein said plant cell is a cotton fiber cell.

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38. (Reiterated) A plant cell comprising a DNA construct of Claim 36.

39. (Reiterated) A plant comprising a plant cell of Claim 38.

Cancel Claims 40 and 41.

*Sub D4*  
42. (Amended) The DNA sequence according to Claim [30] 59 wherein said plant fiber tissue is cotton fiber tissue.

43. (Amended) The DNA sequence according to Claim 42 wherein said transcription factor is selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 7, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 15 and SEQ ID NO: 16.

*C3*  
*Sub D5*  
44. (Amended) A DNA sequence comprising as operably joined components in the direction of transcription, a transcriptional factor functional in a cotton fiber cell and an open reading frame encoding an enzyme in a biosynthetic or degradation pathway of melanin or indigo, wherein said transcriptional factor is obtained by the method of probing a genomic library derived from a plant fiber tissue with up to the full length of a probe derived from the cDNA sequence shown in SEQ ID NO: 1 or SEQ ID NO: 7 or SEQ ID NO: 11 or SEQ ID NO: 12 or SEQ ID NO: 16, wherein hybridization is carried out in a solution comprising 50% formamide, 5X SSC, 0.1% SDS, 5 mM EDTA, 10X Denhardt's solution, and 25 mM sodium phosphate at pH 6.5 with 250 µg/ml carrier DNA, and hybridization washes are performed in 2X SSC, 0.1% SDS at 42°C for 3 x 30 minutes.

45. (Reiterated) The DNA sequence according to Claim 44, further comprising a transport signal encoding sequence from a plant nuclear-encoded gene.

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46. (Reiterated) The DNA sequence according to Claim 45, wherein said transport signal encoding sequence comprises a plastid transit peptide.

47. (Reiterated) The DNA sequence according to Claim 44, further comprising a transport signal encoding sequence for a signal peptide which provides for transport across the rough endoplasmic reticulum.

48. (Reiterated) The DNA sequence according to Claim 47, wherein said sequence further comprises, 3' to said open reading frame, a vacuolar localization signal.

49. (Reiterated) The DNA sequence of Claim 44 wherein said open reading frame is from a bacterial gene.

50. (Reiterated) The DNA sequence of Claim 49 wherein said gene is selected from the group consisting of ORF438, *tyrA*, *pig*, and *tna*.

51. (Reiterated) A DNA construct comprising a DNA sequence of Claim 44.

52. (Reiterated) The DNA construct of Claim 51 wherein said plant cell is a cotton fiber cell.

53. (Reiterated) A plant cell comprising a DNA construct of Claim 51.

54. (Reiterated) A plant comprising a plant cell of Claim 53.

55. (Reiterated) The DNA sequence according to Claim 44 wherein said plant fiber tissue is cotton fiber tissue.

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56. (Reiterated) The DNA sequence according to Claim 55 wherein said transcription factor is selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 7, or SEQ ID NO: 16.

C6 57. (Amended) A DNA sequence comprising as operably joined components in the direction of transcription, a transcriptional factor functional in a cotton fiber cell and an open reading frame encoding an enzyme in the biosynthetic pathway of a pigment, wherein said transcriptional factor is obtained by the method of probing a genomic library derived from a plant fiber tissue with up to the full length of a probe derived from the cDNA sequence shown in SEQ ID NO: 1 or SEQ ID NO: 7 or SEQ ID NO: 16, wherein hybridization is carried out in a solution comprising 50% formamide, 5X SSC, 0.1% SDS, 5 mM EDTA, 10X Denhardt's solution, and 25 mM sodium phosphate at pH 6.5 with 250 µg/ml carrier DNA, and hybridization washes are performed in 2X SSC, 0.1% SDS at 42°C for 3 x 30 minutes.

Please add the following claims:

Sub D20 C7 --58. (New) The DNA sequence according to Claim 28 wherein said transcriptional factor is selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 7, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 15 and SEQ ID NO: 16.

59. (New) A DNA sequence comprising a transcriptional factor functional in a cotton fiber cell, wherein said transcriptional factor is obtained by the method of probing a genomic library derived from a plant fiber tissue with up to the full length of a probe derived from a cDNA sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 7, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 15 and SEQ ID NO: 16, wherein hybridization is carried out in a solution comprising 50% formamide, 5X SSC, 0.1% SDS, 5 mM EDTA, 10X Denhardt's solution, and 25 mM sodium phosphate at pH 6.5 with 250 µg/ml carrier DNA, and hybridization washes are performed in 2X SSC, 0.1% SDS at 42°C for 3 x 30 minutes.

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60. (New) The DNA sequence according to Claim 1, wherein said *rac* promoter sequence is selected from the group consisting of Rac 9 and Rac 13.

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p 26  
61. (New) A recombinant DNA construct comprising the cotton tissue transcriptional sequence shown in SEQ ID NO: 11.

62. (New) An isolated DNA comprising the nucleotide sequence shown in SEQ ID NO: 16.

63. (New) A recombinant DNA construct comprising the cotton tissue transcriptional sequence shown in SEQ ID NO: 17.

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64. (New) The method according to Claim 14, wherein said transcriptional factor is obtained by the method of probing a genomic library derived from a plant fiber tissue with up to the full length of a probe derived from a cDNA sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 7, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 15 and SEQ ID NO: 16, wherein hybridization is carried out in a solution comprising 50% formamide, 5X SSC, 0.1% SDS, 5 mM EDTA, 10X Denhardt's solution, and 25 mM sodium phosphate at pH 6.5 with 250 µg/ml carrier DNA, and hybridization washes are performed in 2X SSC, 0.1% SDS at 42°C for 3 x 30 minutes.--.

### REMARKS

#### The Claimed Invention

The claimed invention is directed to methods for modifying fiber phenotype in a cotton plant, together with DNA sequences and constructs for use in the method and plant cells and plants produced using the method.